DATE: 03/21/2001

TIME: 15:27:37

1645

RAW SEQUENCE LISTING PATENT APPLICATION: US/09/471,255

Input Set : A:\ES.txt

Output Set: N:\CRF3\03212001\I471255.raw

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ENTERED
      4 <110> APPLICANT: BIOCHEM PHARMA INC.
      5
             HAMEL, Jos, e
      6
             BRODEUR, Bernard R.
             PINEAU, Isabelle
             MARTIN, Denis
             RIOUX, Cl, ment
     11 <120> TITLE OF INVENTION: NOVEL STREPTOCOCCUS ANTIGENS
     14 <130> FILE REFERENCE: 12806-11PCT
C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/471,255
C--> 16 <141> CURRENT FILING DATE: 1999-12-23
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     25 <212> TYPE: DNA
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     28 <220> FEATURE:
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        aat aag gac aat aat cgt gtc tct tat gtg gat ggc agc cag tca agt
       cag aaa agt gaa aac ttg aca cca gac cag gtt agc cag aaa gaa gga
                                                                             192
       att cag gct gag caa att gta atc aaa att aca gat cag ggc tat gta
        acg tca cac ggt gac cac tat cat tac tat aat ggg aaa gtt cct tat
       gat gcc ctc ttt agt gaa gaa ctc ttg atg aag gat cca aac tat caa
    39 ctt aaa gac gct gat att gtc aat gaa gtc aag ggt ggt tat atc atc
    40 aag gtc gat gga aaa tat tat gtc tac ctg aaa gat gca gct cat gct
    41 gat aat gtt cga act aaa gat gaa atc aat cgt caa aaa caa gaa cat
    42 gtc aaa gat aat gag aag gtt aac tct aat gtt gct gta gca agg tct
    43 cag gga cga tat acg aca aat gat ggt tat gtc ttt aat cca gct gat
       att atc gaa gat acg ggt aat gct tat atc gtt cct cat gga ggt cac
        tat cac tac att ccc aaa agc gat tta tct gct agt gaa tta gca gca
                                                                             672
        gct aaa gca cat ctg gct gga aaa aat atg caa ccg agt cag tta agc
    47
        tat tct tca aca gct agt gac aat aac acg caa tct gta gca aaa gga
    48
        tca act age aag eea gea aat aaa tet gaa aat ete eag agt ett ttg
        aag gaa ctc tat gat tca cct agc gcc caa cgt tac agt gaa tca gat
                                                                             864
       ggc ctg gtc ttt gac cct gct aag att atc agt cgt aca cca aat gga
                                                                             912
       gtt gcg att ccg cat ggc gac cat tac cac ttt att cct tac agc aag
                                                                             960
       ctt tct gct tta gaa gaa aag att gcc aga atg gtg cct atc agt gga
                                                                            1008
       act ggt tct aca gtt tct aca aat gca aaa cct aat gaa gta gtg tct
       agt cta ggc agt ctt tca agc aat cct tct tct tta acg aca agt aag
    55 gag ctc tct tca gca tct gat ggt tat att ttt aat cca aaa gat atc
       gtt gaa gaa acg gct aca gct tat att gta aga cat ggt gat cat ttc
       cat tac att cca aaa tca aat caa att ggg caa ccg act ctt cca aac
    58 aat agt cta gca aca cct tct cca tct ctt cca atc aat cca gga act
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60 att atc gct gaa gat gaa tca ggt ttt gtc atg agt cac gga gac cac
                                                                         1392
61 aat cat tat ttc ttc aag aag gac ttg aca gaa gag caa att aag gct
62 gcg caa aaa cat tta gag gaa gtt aaa act agt cat aat gga tta gat
63 tet ttg tea tet eat gaa eag gat tat eea ggt aat gee aaa gaa atg
64 aaa gat tta gat aaa aac atc gaa gaa aaa att gct ggc att atg aaa
65 caa tat ggt gtc aaa cgt gaa agt att gtc gtg aat aaa gaa aaa aat
66 gcg att att tat ccg cat gga gat cac cat cat gca gat ccg att gat
67 gaa cat aaa ccg gtt gga att ggt cat tct cac agt aac tat gaa ctg
                                                                         1728
68 ttt aaa ccc gaa gaa gga gtt gct aaa aaa gaa ggg aat aaa gtt tat
                                                                         1776
69 act gga gaa gaa tta acg aat gtt gtt aat ttg tta aaa aat agt acg
                                                                         1824
70 ttt aat aat caa aac ttt act cta gcc aat ggt caa aaa cgc gtt tct
                                                                         1872
71 ttt agt ttt ccg cct gaa ttg gag aaa aaa tta ggt atc aat atg cta
72 gta aaa tta ata aca cca gat gga aaa gta ttg gag aaa gta tct ggt
                                                                         1920
                                                                         1968
73 aaa gta ttt gga gaa gga gta ggg aat att gca aac ttt gaa tta gat
                                                                         2016
74 caa cct tat tta cca gga caa aca ttt aag tat act atc gct tca aaa
                                                                         2064
75 gat tat cca gaa gta agt tat gat ggt aca ttt aca gtt cca acc tct
                                                                         2112
76 tta gct tac aaa atg gcc agt caa acg att ttc tat cct ttc cat gca
                                                                         2160
77 ggg gat act tat tta aga gtg aac cct caa ttt gca gtg cct aaa gga
78 act gat gct tta gtc aga gtg ttt gat gaa ttt cat gga aat gct tat
79 tta gaa aat aac tat aaa gtt ggt gaa atc aaa tta ccg att ccg aaa
80 tta aac caa gga aca acc aga acg gcc gga aat aaa att cct gta acc
                                                                         2352
81 ttc atg gca aat gct tat ttg gac aat caa tcg act tat att gtg gaa
                                                                         2400
82 gta cct atc ttg gaa aaa gaa aat caa act gat aaa cca agt att cta
                                                                         2448
83 cca caa ttt aaa agg aat aaa gca caa gaa aac tca aaa ctt gat gaa
                                                                         2496
84 aag gta gaa gaa cca aag act agt gag aag gta gaa aaa gaa aaa ctt
                                                                         2544
85 tct gaa act ggg aat agt act agt aat tca acg tta gaa gaa gtt cct
86 aca gtg gat cct gta caa gaa aaa gta gca aaa ttt gct gaa agt tat
87 ggg atg aag cta gaa aat gtc ttg ttt aat atg gac gga aca att gaa
                                                                         2688
88 tta tat tta cca tca gga gaa gtc att aaa aag aat atg gca gat ttt
                                                                         2736
89 aca gga gaa gca cet caa gga aat ggt gaa aat aaa eea tet gaa aat
                                                                         2784
90 gga aaa gta tot act gga aca gtt gag aac caa cca aca gaa aat aaa
91 cca gca gat tct tta cca gag gca cca aac gaa aaa cct gta aaa cca
92 gaa aac tca acg gat aat gga atg ttg aat cca gaa ggg aat gtg ggg
93 agt gac cct atg tta gat cca gca tta gag gaa gct cca gca gta gat
94 cct gta caa gaa aaa tta gaa aaa ttt aca gct agt tac gga tta ggc
                                                                         3024
95 tta gat agt gtt ata ttc aat atg gat gga acg att gaa tta aga ttg
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96 cca agt gga gaa gtg ata aaa aag aat tta tct gat ttc ata gcg
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97 taa
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100 <211> LENGTH: 1039
101 <212> TYPE: PRT
102 <213> ORGANISM: S. pneumoniae
104 <400> SEQUENCE: 2
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106
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107
    Ser Leu Ser Leu Cys Ala Tyr Ala Leu Asn Gln His Arg Ser Gln Glu
108
                                     25
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109 Asn Lys Asp Asn Asn Arg Val Ser Tyr Val Asp Gly Ser Gln Ser Ser

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Input Set : A:\ES.txt
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110			35					4.0					4 5			
110	Q1 -	T		C1	7	т	m la aa	40	7	C1	17-1	C	45	r	01	a1
111	GIN	Lys	ser	GIU	ASII	Leu		Pro	ASP	GIII	Val		GIN	ràs	GIU	GIÀ
112		50		0.1	~ 1	1	55	- 1	_	- 1	1	60	a.1		_	
113		Gln	Ala	GIU	GIn		Val	He	Lys	lle		Asp	GIn	Gly	Tyr	
114	65					70					75					80
115	Thr	Ser	His	GIY	_	His	Tyr	His	Tyr	-	Asn	Gly	Lys	Val		Tyr
116					85					90					95	
117	Asp	Ala	Leu		Ser	Glu	Glu	Leu	Leu	Met	Lys	Asp	Pro	Asn	Tyr	Gln
118				100					105					110		
119	Leu	Lys	Asp	Ala	Asp	Ile	Val	Asn	Glu	Val	Lys	Gly	Gly	Tyr	Ile	Ile
120			115					120					125			
121	Lys	Val	Asp	Gly	Lys	Tyr	Tyr	Val	Tyr	Leu	Lys	Asp	Ala	Ala	His	Ala
122		130					135					140				
123	Asp	Asn	Val	Arg	Thr	Lys	Asp	Glu	Ile	Asn	Arg	Gln	Lys	Gln	Glu	His
124	145					150					155					160
125	Val	Lys	Asp	Asn	Glu	Lys	Val	Asn	Ser	Asn	Val	Ala	Val	Ala	Arg	Ser
126					165					170					175	
127	Gln	Gly	Arg	Tyr	Thr	Thr	Asn	Asp	Gly	Tyr	Val	Phe	Asn	Pro	Ala	Asp
128				180				-	185	-				190		
129	Ile	Ile	Glu	Asp	Thr	Gly	Asn	Ala	Tyr	Ile	Val	Pro	His	Gly	Gly	His
130			195	_		_		200	-				205	_	_	
131	Tyr	His	Tyr	Ile	Pro	Lys	Ser	Asp	Leu	Ser	Ala	Ser	Glu	Leu	Ala	Ala
132	-	210	-			-	215	•				220				
133	Ala	Lys	Ala	His	Leu	Ala	Glv	Lvs	Asn	Met	Gln	Pro	Ser	Gln	Leu	Ser
134	225	1				230	1				235					240
135	Tvr	Ser	Ser	Thr	Ala	Ser	Asp	Asn	Asn	Thr		Ser	Va l	Ala	Lvs	G1v
136					245					250					255	2
137	Ser	Thr	Ser	Lvs		Ala	Asn	Lvs	Ser		Asn	Len	Gln	Ser		Len
138				260				-1-	265					270		
139	Lvs	Glu	T.eu		Asp	Ser	Pro	Ser		Gln	Δra	Tvr	Ser		Ser	Asp
140	<i>D</i> ₁ <i>O</i>	014	275	-1-	шр	001		280	mu	01	9	-1-	285	014	DCI	p
141	Glv	Leu		Phe	Asp	Pro	Δla		Tle	Tle	Ser	Ara		Pro	Asn	G1 v
142	01	290	,		op	110	295	D _I S	110	110	001	300	1111	110	21011	011
143	Va 1	Ala	Tle	Pro	His	Glv		His	ጥህዮ	His	Phe		Pro	Tur	Ser	Lvs
144	305					310	···op		+1-		315	110	110	-1-	OCI	320
145		Ser	Δla	I.e.ii	Glu		Lvs	Tle	Δla	Δrσ		Va 1	Pro	Tle	Ser	
146	LCu	UCI	111u	шси	325	Oru	цуэ	110	niu	330	rict	VUI	110	110	335	OLY
147	Thr	Gly	Ser	Thr		Ser	Thr	Δen	Δla		Dro	Δen	Glu.	Val		Sar
148	T 11T	OLY	JCI	340	vuı	DCI	1111	กวแ	345	цуз	110	USII	Giu	350	Val	Jei
149	Sar	Leu	Cl v		Τ.Δ11	Sar	Sar	λen		Sar	Sor	Lon	Thr		Cor	Lvc
150	Der	neu	355	261	шеи	Ser	261	360	FIU	261	261	пеп	365	1111	261	шуз
151	Clu	Lou		Cor	712	cor	λαη		m	т1а	Dho	7 an		T	λan	т10
152	Giu	Leu 370	261	361	мта	ser	375	GIY	тут	116	Phe		PIO	гуу	ASP	116
153	17 a 1		C1	mhm	7.1.0	mba		Mex.	T1-	17.0 1	7 ~-	380	C1	7	rr 2 -	Dha
		Glu	GIU	1111	Ата		Ald	TAL	тте	val	_	HIS	GTÄ	ASP	HIS	
154	385	M	т1 ~	Dro	T •• ~	390	7. ~ ~	C1 =	т1 -	C1	395	D	m l	T = · ·	D	400
155	птэ	Tyr	116	LT.O	_	ser	ASII	GTII	тте	-	GTU	LT.O	THE	ьeu		ASII
156	7	C	т	71-	405	D	G + -	D	0	410	D	т1 -		_	415	m la
157	ASI	Ser	ьeu		rnr	PLO	ser	Pro		ьeu	PIO	тте	Asn		стλ	rnr
158				420					425					430		

RAW SEQUENCE LISTING
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159	Ser	His		Lys	His	Glu	Glu		Gly	Tyr	Gly	Phe		Ala	Asn	Arg
160	- 1	-1.	435	0 1	•	~ 1	<u> </u>	440	5 1	,			445	~ 1	_	
161	ile		Ala	GIU	Asp	GLU		GLY	Pne	vai	Met		HIS	Gly	Asp	HIS
162	7	450	Merm	Dho	Dho	T 0	455	7	T 0.13	III la sa	C1	460	C1 n	т1а	T	77-
163 164	465	HIS	TAT	File	Pile	470	ьуѕ	ASP	Leu	THE	475	GIU	GIII	Ile	гуу	480
165		Cln	Tuc	uic	T Ou		C1.,	W - 1	Trra	Пhх		изс	A can	Gly	Tan	
166	ALG	GIII	пуз	пто	485	Gru	GIU	Val	цуз	490	Ser	1172	ASII	СТУ	495	кър
167	Ser	Len	Ser	Ser		Glu	Gln	Asn	ጥህጉ		Glv	Δsn	Δla	Lys		Met
168	501		501	500			0111		505		0.1			510	010	1100
169	Lys	Asp	Leu		Lys	Lys	Ile	Glu		Lys	Ile	Ala	Gly	Ile	Met	Lys
170	-	•	515	-	-	•		520		-			525			-
171	Gln	Tyr	Gly	Val	Lys	Arg	Glu	Ser	Ile	Val	Val	Asn	Lys	Glu	Lys	Asn
172		530					535					540				
173	Ala	Ile	Ile	Tyr	Pro	His	Gly	Asp	His	His	His	Ala	Asp	Pro	Ile	Asp
174	545					550					555					560
175	Glu	His	Lys	Pro		Gly	Ile	Gly	His		His	Ser	Asn	Tyr		Leu
176					565					570					575	
177	Phe	Lys	Pro		Glu	Gly	Val	Ala		Lys	Glu	Gly	Asn	Lys	Val	Tyr
178	1	- 1	~ 1	580	_	1	_		585	_	_	_	_	590		
179	Thr	Gly		Glu	Leu	Thr	Asn		Val	Asn	Leu	Leu	-	Asn	Ser	Thr
180	Dha	7 ~~	595	<i>a</i> 1 -	7	Dho	m b so	600	7 l n	7 ~ ~	C1	C1 -	605	7 ~~ ~	37- 1	Con
181 182	Pne	610	ASN	GIN	ASI	Pne	615	Leu	Ата	ASN	GTÀ	620	гàг	Arg	vaı	ser
183	Dho		Dho	Pro	Pro	Clu		Clu	Luc	Luc	Lau		Tla	Asn	Mot	Lau
184	625	Ser	riie	FIU	rio	630	цеа	GIU	пуз	цуз	635	GIY	116	ASII	nec	640
185		Lvs	Leu	Tle	Thr		Asp	Glv	Lvs	Va 1		Glu	Lvs	Val	Ser	
186		-12			645		110 [011	_10	650		014	_70		655	0-1
187	Lys	Val	Phe	Gly	Glu	Gly	Val	Gly	Asn		Ala	Asn	Phe	Glu	Leu	Asp
188	-			660		-		-	665					670		-
189	Gln	Pro	Tyr	Leu	Pro	Gly	Gln	Thr	Phe	Lys	Tyr	Thr	Ile	Ala	Ser	Lys
190			675					680					685			
191	Asp	Tyr	Pro	Glu	Val	Ser	Tyr	Asp	Gly	Thr	Phe	Thr	Val	Pro	Thr	Ser
192		690					695					700				
193		Ala	Tyr	Lys	Met		Ser	Gln	Thr	Ile		Tyr	Pro	Phe	His	
194	705	_				710	•	_	_	_,	715			_	_	720
195	GLy	Asp	Thr	Tyr		Arg	Val	Asn	Pro		Phe	Ala	Val	Pro		Gly
196	m)	3	31-	T	725		37- 1	D1		730	Dl	***	01		735	m
197 198	Thr	Asp	Ата	140	vaı	Arg	vaı	Pne	745	GIU	Phe	HIS	GLY	Asn 750	Ата	Tyr
199	Ť OU	Clu	7 cn		Пттх	T 110	W-1	C 1 + r		Tlo	Tuc	Lou	Dro	Ile	Dro	T ***
200	пец	Giu	755	ASII	TÀT	цуз	vaı	760	GIU	116	пуз	Leu	765	116	FIU	цуѕ
201	Len	Asn		Glv	Thr	Thr	Arσ		Δla	Glv	Δsn	T.vc		Pro	Va 1	Thr
202	200	770	01	4 1 1			775		114.00	011	11011	780		110	, 41	1111
203	Phe		Αla	Asn	Ala	Tvr		Asp	Asn	Gln	Ser		Τvr	Ile	Va 1	Glu
204	785					790		F			795		- 4 -			800
205		Pro	Ile	Leu	Glu	Lys	Glu	Asn	Gln	Thr	Asp	Lys	Pro	Ser	Ile	
206					805	-				810	-	_			815	
207	Pro	Gln	Phe	Lys	Arg	Asn	Lys	Ala	Gln	Glu	Asn	Ser	Lys	Leu	Asp	Glu

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209	Lvc	Val	Glu		Pro	Lys	Thr	Ser		T.VS	Val	Glu	Lvs		Lys	Len	
210	11,5	,	835	0 u		_, _		840	O_u	1 1 2	,	014	845	V u	<i>L</i> ₁ <i>S</i>	шса	
211	Ser	Glu		Glv	Asn	Ser	Thr		Asn	Ser	Thr	T.e.ii	_	Glu	Val	Pro	
212	Ser	850	1111	OLY	11011	501	855	DCI	71511	DCI	1111	860	Olu	OIU	Val	110	
213	Thr		Nen	Dro	Wa l	Gln		Lvc	Val	7 l a	Twe		λla	G1n	Ser	Ttr	
214	865	Val	мэр	FIU	val	870	Olu	шуз	var	Ата	875	FILE	лта	GIU	Ser	880	
215		Mot	T	T 011	Clu		3/ n 1	T OU	Dho	λον		700	Cly	Thr	Ile		
215	GIY	Met	ryys	neu	885	MSII	vai	Leu	rne	890	met	ASP	GIY	1111	895	GIU	
	T	M****	T 0	Dwa		C1	C1	3/23	T10		T *** G	1 an	Mat	7 1 a		Dha	
217	Leu	TYL	Leu	900	261	GTY	GLU	Vai	905	гуѕ	гìх	ASII	мес	910	Asp	Pne	
218	m 1	C1	~1		D	C1 -	C1	1		C1	3	T	D.m.o.		G1	N	
219	THE	GTĀ		Ald.	PIO	GIII	GTA		GTĀ	GIU	ASII	rλz		ser	Glu	ASII	
220	01	T	915	a	m 1	a1	m 1	920	a1	3	01	D	925	01	3	Ť	
221	GIY	_	val	Ser	Thr	GTÄ		vaı	GIU	ASN	GIN		rnr	GIU	Asn	гàг	
222	_	930			-	_	935		ъ.		0.1	940	_	1	_	_	
223	4	АТА	Asp	Ser	Leu		GLu	АТа	Pro	Asn		Lys	Pro	vaı	Lys		
224	945		_	_,		950	~ 1		_	_	955			_		960	
225	Glu	Asn.	Ser	Thr	_	Asn	GIA	Met	Leu		Pro	Glu	GTA	Asn	Val	GLY	
226					965			_		970	_	_			975		
227	Ser	Asp	Pro		Leu	Asp	Pro	Ala		Glu	Glu	Ala	Pro		Val	Asp	
228				980					985					990			
229	Pro	Val		Glu	Lys	Leu	Glu	_		Thr	Ala	Ser	Tyr	Gly	Leu	Gly	
230			995					1000)				1005	5			
231	Leu	Asp	Ser	Val	Ile	Phe	Asn	Met	Asp	Gly	Thr	Ile	Glu	Leu	Arg	Leu	
222		1010)				1015	5				1020)				
232		1010	,														
233	Pro			Glu	Val	Ile	Lys		Asn	Leu	Ser	Asp	Phe	Ile	Ala		
233 234	1025	Ser	Gly			Ile 1030	Lys		Asn	Leu	Ser 1035	-	Phe	Ile	Ala		
233 234		Ser	Gly				Lys		Asn	Leu		-	Phe	Ile	Ala		
233 234 236	1025	Ser SEQ	Gly O ID	NO:	3		Lys		Asn	Leu		-	Phe	Ile	Ala		
233 234 236 237	1025	Ser SEQ	Gly O ID NGTH:	NO: 252	3		Lys		Asn	Leu		-	Phe	Ile	Ala		
233 234 236 237 238	1025 <210> <211>	Ser SEQ LEN TYP	Gly ID GTH: PE: I	NO: 252 NA	3 23	1030	Lys)	Lys	Asn	Leu		-	Phe	Ile	Ala		
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